

Clean Version of Page 11, Paragraph 4**METHOD TO ALTER LEVELS OF A DNA REPAIR PROTEIN (as amended)**

Applicant: John H.J. Petrini et al.

Serial No.: Unknown

Figure 6. Structure of the p95 cDNA. (A) The schematic diagram represents the structure of the p95 cDNA. The entire 4,483 basepair (bp) cDNA is represented by the thin line and the rectangular box is the 754 amino acid (aa) open reading frame (ORF) (SEQ ID NO:2). Within the ORF the grey box indicates the N-terminal region showing homology to *S. cerevisiae* Xrs2. The solid line above the ORF indicates the region cloned by two-hybrid screen utilizing hMre11 as bait. (B) N-terminal alignment of p95 (SEQ ID NO:3) with Xrs2 (SEQ ID NO:4). The shaded boxes indicate the regions of similarity. The two proteins show 28% identity and 46% similarity over the region displayed. The following amino acids were considered similar: {D, E, N, Q} {F, W, Y} {I, L, V} {K, R} {A, G} {S, T} {C} {H} {M} {P}. (C) A Zoo-Blot Southern blot (Clontech, Palo Alto, CA) of EcoRI digested DNA from various species was probed with the *NBS1* cDNA. Lane 1, human; lane 2, monkey; lane 3, rat; lane 4, mouse; lane 5, dog; lane 6, cow; lane 7, rabbit; lane 8, chicken; and lane 9, yeast. The position of size markers (in kilobase pairs) is indicated on the left.

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Figure 14. cDNA sequence of p95 (SEQ ID NO:1).

Clean Version of Page 73, Table 1**METHOD TO ALTER LEVELS OF A DNA REPAIR PROTEIN (as amended)**

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Table 1
Peptides Obtained From Mass Spectrometry Analysis

Peptide ^a	Position ^b
-QPPQIESFYPPPLDEPSIGSK-	189-209 (SEQ ID NO:9)
-LSSAVVFGGGEAR-	238-251 (SEQ ID NO: 10)
-WIQSIMDMLQR-	289-299 (SEQ ID NO: 11)
-QGLRPIPEAEIGLAVIFMTTK-	300-320 (SEQ ID NO: 12)
-TTTPGPSLSQGVSVDEK-	335-351 (SEQ ID NO: 13)
-MLSQDAPTVKE-	395-404 (SEQ ID NO: 14)
-TSSNNNSMVSNTLAK-	409-423 (SEQ ID NO: 15)
-IPNYQLSPTKLPSINK-	426-441 (SEQ ID NO: 16)
-NYFQPSTKK-	458465 (SEQ ID NO:17)
-NKEQHLSENEPVDTNSDNNLFTDTDLK-	503-529 (SEQ ID NO:18)
-EMDDVAIEDEVLEQLFK-	552-558 (SEQ ID NO: 19)
-MDIETNDTFSDEAVPESSK-	595-613 (SEQ ID NO:20)
-ELKEDSWAK-	625-635 (SEQ ID NO: 21)
-KLLLTEFR-	653-660 (SEQ ID NO:22)
-NPSGINDDYGQLK- ^c	671-683 (SEQ ID NO:23)
-EESLADDLFR-	736-745 (SEQ ID NO:24)